CLAIM AMENDMENTS

1. (previously presented) Nucleic acids coded for a deregulated 3-phosphoglycerate dehydrogenase containing a gene serA according to SEQ ID No. 1 or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

2. (previously presented) Nucleic acids coding for a deregulating 3-phosphoglycerate dehydrogenase containing a gene *serA* according to SEQ ID No. 2 or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

3. (previously presented) Nucleic acids coding for a deregulating 3-phosphoglycerate dehydrogenase containing a gene *serA* according to SEQ ID No. 3 or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

4. (previously presented) Nucleic acids coding for a deregulating 3-phosphoglycerate dehydrogenase containing a gene *serA* according to SEQ ID No. 4 or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

5. (previously presented) Nucleic acids coding for a deregulating 3-phosphoglycerate dehydrogenase containing a gene *serA* according to SEQ ID No. 5 or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

6. (previously presented) Nucleic acids according to one of claims 1 to 5 characterized in that they are isolated from coryneform bacteria.

7. (previously presented) Nucleic acids according to one of claims 1 to 6 characterized in that they are isolated from Corynebacterium or Brevibacterium.

8. (previously presented) Nucleic acids according to one of claims 1 to 7 characterized in that they are isolated *Corynebacterium glutamicum* or *Brevibacterium flavum*.

9. (previously presented) A gene structure containing at least one of the nucleotide sequences according to claims 1 to 8 as well as regulatory sequences operatively linked therewith.

10. (previously presented) A vector containing at least one nucleotide sequence according to claims 1 to 8 or a gene structure according to claim 9 as well as additional nucleotide

sequence for selection, replication in the host cell or for interaction in the host cell genome.

11. (previously presented) A deregulated 3-phosphoglycerate-dehydrogenase or a part thereof loaded by means of a nucleic acid sequence according to one of the claims 1 to 8.

12. (previously presented) A deregulated 3-phosphoglycerate-dehydrogenase according to claim 11 with an amino acid sequence according to SEQ ID No. 7 or a modified form of this polypeptide sequence or isoform thereof.

13. (previously presented) A deregulated 3-phosphoglycerate-dehydrogenase according to claim 11 with an amino acid sequence according to SEQ ID No. 8 or a modified form of this polypeptide sequence or isoform thereof.

14. (previously presented) A deregulated 3-phosphoglycerate-dehydrogenase according to claim 11 with an amino acid sequence according to SEQ ID No. 9 or a modified form of this polypeptide sequence or isoform thereof.

15. (previously presented) A deregulated 3-phosphoglycerate-dehydrogenase according to claim 11 with an amino acid sequence according to SEQ ID No. 10 or a modified form of this polypeptide sequence or isoform thereof.

16. (previously presented) A deregulated 3-phosphoglycerate-dehydrogenase according to claim 12 with an amino acid sequence according to SEQ ID No. 11 or a modified form of this polypeptide sequence or isoform thereof.

17. (previously presented) A polypeptide according to one of claims 11 to 16 characterized in that it derives from coryneform bacteria.

18. (previously presented) A polypeptide according to one of the claims 11 to 17 characterized in that it derives from Corynebacterium or Brevibacterium.

19. (previously presented) A polypeptide according to one of the claims 11 to 18 characterized in that it derives from *Corynebacterium glutamicum* or *Brevibacterium flavum*.

20. (previously presented) A microorganism containing at least one nucleic acid according to claims 1 to 8 in replicatable form and which by comparison with the wild type microorganism is expressed in an amplified manner and/or has its copy number increased.

21. (previously presented) A microorganism according to claim 20 containing in replicable form a gene structure according to claim 9 or a vector according to claim 10.

22. (previously presented) A microorganism according to one of the claims 20 to 21 containing at least one polypeptide according to claims 11 to 19 which, by comparison to the corresponding wild type line shows an active deregulated 3-phosphoglycerate-dehydrogenase.

23. (previously presented) The microorganism according to one of the claims 20 to 22 characterized in that it is a Coryneform bacterium.

24. (previously presented) The microorganism according to one of claims 20 to 23 characterized in that it belongs to the familia Corynebacterium or Brevibacterium.

25. (previously presented) The microorganism according to one of claims 20 to 24 characterized in that it belongs to *Corynebacterium glutamicum* or *Brevibacterium flavum*.

26. (previously presented) A probe for identifying and/or isolating genes coded for proteins participating in the biosynthesis of L-serine characterized in that they are made

starting from nucleic acids according to one of the claims 1 to 8 and containing a marker suitable for detection.

27. (Currently amended) The method for microbial production of ~~L-serin~~ L-serine characterized in that

a) at least one nucleic acid according to one of the claims 1 to 8 is isolated from a coryneform bacterium and is translated in a microorganism and there expressed, whereby the gene expression and/or the activity of the corresponding coded polypeptide is increased with respect to the corresponding microorganism which has not been genetically altered;

b) this genetically modified microorganism from step a) is used for microbial production; and

c) the correspondingly formed L-serine is isolated from the culture medium.

28. (new) A method for microbially producing L-serine from a carbohydrate, fat or oil, fatty acid, alcohol or organic acid, in a culture medium, containing nitrogen sources and phosphorous sources, which comprises the steps of:

a) providing at least one nucleic acid coding for a deregulating 3-phosphoglycerate dehydrogenase, and selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5,isolated from a Coryneform bacterium, and translated into a Coryneform bacterium, and then expressed to form the deregulating 3-phosphoglycerate dehydrogenase, whereby the

gene expression and/or the activity of the corresponding coded deregulating 3-phosphoglycerate dehydrogenase is increased with respect to the corresponding microorganism which has not been genetically altered;

b) microbially producing L-serine by expressing the at least one nucleic acid coding for a deregulating 3-phosphoglycerate dehydrogenase in said genetically modified microorganism from step a) to microbially convert said carbohydrate, fat or oil, fatty acid, alcohol or organic acid in said culture medium to L-serine; and

c) isolating the correspondingly formed L-serine from the culture medium.

29. (New) The method for microbially producing L-serine from a carbohydrate, fat or oil, fatty acid, alcohol or organic acid, in a culture medium, defined in claim 28 wherein the nucleic acid coding for a deregulating 3-phosphoglycerate dehydrogenase is SEQ ID NO: 1.